AMENDMENTS TO THE CLAIMS

This following listing of claims is provided as a courtesy. No amendments are made at this time.

Claim 1. (withdrawn) A method of detecting infectious disease minority variants, comprising:

contacting a nucleic acid sample from a subject or a cell with at least one oligonucleotide pair to form a reaction mixture, wherein a pair comprises a first (P1) and a second (P2) oligonucleotide, wherein P1 comprises a first gene specific region and a first primer region, P2 comprises a second gene specific region and a second primer region; either P1 or P2 comprise a detection region; either P1 or P2 comprise a nucleotide difference in the gene specific region; and P1 and P2 are suitable for ligation to one another;

subjecting the reaction mixture to a ligation reaction; and

amplifying a ligation product to form a reaction product.

Claim 2. (withdrawn) The method of claim 1, wherein the minority variant is viral or microbial.

Claim 3. (withdrawn) The method of claim 1, wherein the viral minority variant is HIV, HBV, HCV, CMV, influenza, HSV, RSV, or VZV.

Claim 4. (withdrawn) The method of claim 3, wherein the viral minority variant is a viral drug-resistant minority variant.

Claim 5. (withdrawn) The method of claim 1, wherein the nucleotide difference detected encodes one or more of the amino acid changes K103N, Y181C, K103E, K103R, K103T, G190A, P236L, or another substitution in the viral genome associated with altered susceptibility to one or more antiviral drugs.

Claim 6. (previously presented) A method of differentiating pancreatic cancer from chronic pancreatitis comprising:

contacting a nucleic acid sample from a human subject or a cell with at least one oligonucleotide pair to form a reaction mixture, wherein a pair comprises a first (P1) and a second (P2) oligonucleotide, wherein P1 comprises a first gene specific region and a first primer region, P2 comprises a second gene specific region and a second primer region; either P1 or P2 comprise a detection region; either P1 or P2 comprise a nucleotide difference in the gene specific region wherein the gene is KRAS2 and the nucleotide difference comprises at least one of a G35A, a G35T, or a G34 C nucleotide substitution; and P1 and P2 are suitable for ligation to one another;

subjecting the reaction mixture to a ligation reaction;

amplifying a ligation product to form a reaction product; and

analyzing the reaction product to quantify the reaction product and determine a mutation level within the nucleic acid sample, wherein the mutation level of KRAS2 is equal to the mutant KRAS2/(mutant KRAS2 + wild-type KRAS2), and

detecting a nucleotide difference in KRAS2, wherein the nucleotide difference comprises at least one of a G35A, a G35T, or a G34 C nucleotide substitution, in the nucleic acid of the human subject differentiates pancreatic cancer from pancreatitis.

Claim 7-10. (cancelled)

Claim 11. (previously presented) The method of claim 6, wherein detecting a nucleotide difference in KRAS2 comprises detecting a mutation level in KRAS2, and wherein a mutation level of less than about 0.6% in KRAS2 indicates chronic pancreatitis.

Claim 12. (previously presented) The method of claim 6, wherein detecting a nucleotide difference in KRAS2 comprises detecting a mutation level in KRAS2, and

wherein a mutation level of from between about 0.5% to about 80% in KRAS2 indicates pancreatic cancer.

Claim 13. (original) The method of claim 6, further comprising monitoring the KRAS mutation levels.

Claim 14-22. (cancelled)

Claim 23. (withdrawn) A method of forensic identification, comprising:

obtaining a nucleic acid forensic sample;

contacting a nucleic acid forensic sample with at least one oligonucleotide pair to form a reaction mixture, wherein a pair comprises a first (P1) and a second (P2) oligonucleotide, wherein P1 comprises a first gene specific region and a first primer region, P2 comprises a second gene specific region and a second primer region; either P1 or P2 comprise a detection region; either P1 or P2 comprise a nucleotide difference in the gene specific region; and P1 and P2 are suitable for ligation to one another;

subjecting the reaction mixture to a ligation reaction; and

amplifying a ligation product to form a reaction product.

Claims 24-27. (cancelled)

Claim 28. (withdrawn) A method of identifying a sample containing an uncommon genetic change, comprising:

obtaining a pooled nucleic acid sample;

contacting the pooled sample with at least one oligonucleotide pair to form a reaction mixture, wherein a pair comprises a first (P1) and a second (P2) oligonucleotide, wherein P1 comprises a first gene specific region and a first primer region, P2 comprises a second gene specific region and a second primer region; either

P1 or P2 comprise a detection region; either P1 or P2 comprise a nucleotide difference in the gene specific region; and P1 and P2 are suitable for ligation to one another;

subjecting the reaction mixture to a ligation reaction; and

amplifying a ligation product to form a reaction product.

Claim 29. (withdrawn) The method of claim 28, wherein the pooled nucleic acid sample is a pool of samples.

Claim 30. (withdrawn) The method of claim 1, wherein the mutated gene specific region is at the 3'end of P1 and/or the 5' end of P2.

Claims 31-39. (cancelled)

Claim 40. (withdrawn) A method of detecting a nucleic acid sequence difference, comprising:

contacting a nucleic acid sample with at least one oligonucleotide pair, wherein a pair comprises a first (P1) and a second (P2) oligonucleotide, wherein P1 and P2 bind to a nucleic acid to form a reaction mixture, and wherein P1 comprises a first gene specific region and a first primer binding region and P2 comprises a probe binding region, a second primer binding region and a second gene specific region, wherein there is a gap of one or more nucleotides between the first and second gene specific regions contains the nucleic acid difference;

providing the reaction mixture with a nucleotide complementary to the nucleotide difference nucleic acid difference;

subjecting P1, P2, and the nucleotide to ligation conditions to form a ligation product; and

amplifying the ligation product to form a reaction product.

Claim 41. (withdrawn) The method of claim 1, wherein the nucleic acid difference is one or more of KRAS2 nucleotide difference, K103N HIV-1 drug-resistance nucleotide difference, CFTR nucleotide difference, p53 nucleotide difference, or Braf nucleotide difference.

Claim 42. (withdrawn) The method of claim 41, wherein the nucleotide ligates to one or more of P1 or P2 if the nucleotide difference is present.

Claims 43-74. (cancelled)

Claim 75. (withdrawn) A kit for one of more of detecting infectious disease minority variants, differentiating pancreatic cancer from chromic pancreatitis, diagnosing a disease, forensic identification, comprising:

at least one first (P1) and at least one second (P2) oligonucleotide to form a reaction mixture, wherein P1 comprises a first gene specific region and a first primer region, P2 comprises a second gene specific region and a second primer region; either P1 or P2 comprise a detection region; either P1 or P2 comprise a nucleotide difference in the gene specific region; and P1 and P2 are suitable for ligation to one another; and

instructions for use.

Claim 76. (withdrawn) A kit for one of more of detecting infectious disease minority variants, differentiating pancreatic cancer from chromic pancreatitis, diagnosing a disease, forensic identification, or detecting a nucleic acid sequence difference, comprising:

at least one first (P1) and at least one second (P2) oligonucleotide, wherein P1 and P2 bind to a nucleic acid to form a reaction mixture, and wherein P1 comprises a first gene specific region and a first primer binding region and P2 comprises a probe binding region, a second primer binding region and a second gene specific region, wherein there a nucleotide gap between the first and second gene specific regions contains the nucleic acid difference; and instructions for use.

Claim 77. (previously presented) The method of claim 6, wherein the sensitivity is at least 76%.

Claim 78. (previously presented) The method of claim 6, wherein the sensitivity is at least 88%.

Claim 79. (previously presented) The method of claim 6, wherein the sensitivity is 94%.

Claim 80. (previously presented) The method of claim 6, wherein either P1 or P2 comprises a foreign DNA region between the gene specific region and the primer region.

Claim 81. (previously presented) The method of claim 80, wherein the foreign DNA region is used as a probe.

Claim 82. (previously presented) The method of claim 6, wherein amplification comprises a method selected from the group consisting of the amplifying is by quantitative polymerase chain reaction (PCR), real time PCR, and real time quantitative PCR.

Claim 83. (previously presented) The method of claim 82, wherein the amplifying comprises a multiplex PCR reaction.

Claim 84. (previously presented) The method of claim 6, wherein a mutation level of 10% or less can be detected.

Claim 85. (previously presented) The method of claim 6, wherein a mutation level of 1% or less can be detected.

Claim 86. (previously presented) The method of claim 6, wherein a mutation level of 0.1% or less can be detected.